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## OM protein - protein search, using sw model

Run on: January 7, 2002, 15:42:01 ; Search time 77.81 Seconds  
(without alignments)  
291.208 Million cell updates/sec

Title: US-08-569-749-2

Perfect score: 3277

Sequence: 1 MRKTAQSRLFPGPSYONIKS.....LRKCPICRGIIKGTVRTFLS 618

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB ID	Description	RESULT [1]
1	3277	100.0	618	1 BIR3_HUMAN	Q13490 homo sapien	BIR3_HUMAN STANDARD; PRT: 618 AA.
2	2728	83.2	612	1 BIR3_MOUSE	Q62210 mus musculus	ID: BIR3_HUMAN STANDARD; PRT: 618 AA.
3	2353	71.8	604	1 BIR2_HUMAN	Q13489 homo sapien	AC: Q13490; Q16516; DT: 01-NOV-1997 (Rel. 35, Created)
4	2233.5	68.1	611	1 BIR2_CHICKEN	Q90660 gallus gallus	DT: 01-NOV-1997 (Rel. 35, Last sequence update)
5	2172	66.3	600	1 BIR2_MOUSE	Q08863 mus musculus	DT: 20-AUG-2001 (Rel. 40, Last annotation update)
6	1532	46.8	358	1 PIAP_PIG	Q62640 sus scrofa	DE: BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (IAP2) (HTAP-2) (C-IAP1) (TNFR2-TAF SIGNALING COMPLEX DE: PROTEIN 2) (TAP HOMOLOG B).
7	911	27.8	497	1 BIR4_HUMAN	P98170 homo sapien	DE: PROTEIN 2) (TAP HOMOLOG B).
8	910	27.8	496	1 BIR4_MOUSE	Q60589 mus musculus	GN: BIRG3 OR API2 OR IAP2 OR MIHB.
9	904.5	27.6	496	1 BIR4_DROME	Q9R016 rattus norvegicus	OS: Homo sapiens (Human).
10	744.5	22.7	498	1 IAP2_DROME	Q24307 drosophila melanogaster	OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11	513	15.7	268	1 IAP3_NVOP	P41437 oryctes pse	NCBI_TaxID:9606;
12	506	15.4	1403	1 BIRE_MOUSE	Q9R016 mus musculus	RN: [1]
13	499.5	15.2	1403	1 BIRF_MOUSE	Q9J1B0 mus musculus	RP: SEQUENCE FROM N.A.
14	498.5	15.2	1402	1 BIRG_MOUSE	Q9J1B3 mus musculus	RX: MEDLINE-96120127; PubMed=8548810;
15	484	14.8	438	1 IAP1_DROME	Q24306 drosophila melanogaster	RT: "The TNFR2-TRAF signalling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";
16	468.5	14.3	1403	1 BIRAL_MOUSE	Q9QK55 mus musculus	RT: Cell 83:1243-1252(1995).
17	468	14.3	1447	1 BIRB_MOUSE	Q9QK44 mus musculus	RN: [2]
18	462	14.1	1403	1 BIRL_HUMAN	Q9J075 homo sapien	RP: SEQUENCE FROM N.A.
19	461	14.1	249	1 IAP1_NVAC	P41436 cydia pomonella	RX: MEDLINE-96149249; PubMed=8552191;
20	238.5	7.3	286	1 IAP1_NVAC	P41435 autographa californica	RC: LISTON P., ROY N., TAMIL K., LEFEBVRE C., BAIRD S., CHERTON-HORVAT G., FARAHANI R., MCLEAN M., IKEDA J., MACKENZIE A., KORNELUK R.G.;
21	237.5	7.2	997	1 BIRL_SCHPO	Q9J077 homo sapien	RA: "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";
22	223	6.8	275	1 IAP1_NVOP	Q9J078 homo sapien	RT: Nature 379:49-353(1996).
23	199.5	6.1	829	1 BIR6_HUMAN	Q9J079 homo sapien	RN: [3]
24	175.5	5.4	239	1 IZP2_IW6	Q9J075 homo sapien	RP: SEQUENCE FROM RETAL LIVER.
25	144	4.4	249	1 IAP2_NVAC	P41435 autographa californica	RX: MEDLINE-96209843; PubMed=8643514;
26	141.5	4.3	142	1 BIR5_RAT	P41435 autographa californica	RC: UREN A.G., PAKUSCH M., HAWKINS C.J., PULS K.L., VAUX D.L.;
27	139	4.2	140	1 BIR5_MOUSE	Q9J074 homo sapien	RT: CLONING AND EXPRESSION OF APOPTOSIS INHIBITORY PROTEIN HOMOLOGS THAT FUNCTION TO INHIBIT APOPTOSIS AND/OR BIND TUMOR NECROSIS FACTOR RECEPTOR-ASSOCIATED FACTORS.;
28	137.5	4.2	140	1 IAP2_NVOP	Q9J076 homo sapien	RT: PROC. NATL. ACAD. SCI. U.S.A. 93:4974-4978(1996).
29	132.5	4.0	490	1 BMD4_HUMAN	Q9J077 homo sapien	RN: [4]
30	131	4.0	142	1 BIR5_HUMAN	Q9J078 homo sapien	RP: STRUCTURE BY NMR OF 266-363.
31	126	3.8	145	1 ZEF2_IW6	P40629 chilo iridota	RX: MEDLINE-99333054; PubMed=10404221;
32	120.5	3.7	834	1 YNC4_CAEEL	P41435 autographa californica	RA: HINDS M.G., NORTON R.S., VAUX D.L., DAY C.L.;
33	3.7		954	1 BIRL YEAST	Q9J079 homo sapien	RT: "SOLUTION STRUCTURE OF A BACULOVIRAL INHIBITOR OF APOPTOSIS (IAP) REPEAT.";
						RT: NAT. STRUCT. BIOL. 6:648-651(1999).
						CC: "-1- FUNCTION: A POTENTIALLY SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAFF1 AND TRAF2) TO FORM AN HETEROGENERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).
						CC: "-1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
						CC: "-1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.
						CC: MAINLY EXPRESSED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY, AND PANCREAS, LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD
						CC: LEUKOCYTES.
						CC: P47134 saccharomyces cerevisiae

CC	-1- SIMILARITY: BELONGS TO THE TAP FAMILY.	Db	361 STSDTGEENADPPLIHFGGESESSEDAMNTVVKSALEMGRNRLVQTVQSKLTT	
CC	-1- SIMILARITY: CONTAINS 3 BIR REPEATS.	Qy	421 GENKYVNDIVSALINADEKREKEKOEAREMASDDLSITRKRMALFQLTCVLPILD	
CC	-1- SIMILARITY: CONTAINS 1 CARD DOMAIN.	Db	421 GENKYVNDIVSALINADEKREKEKOEAREMASDDLSITRKRMALFQLTCVLPILD	
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	Qy	481 NLLKANVINQEHDTIKOKTOPIQOARELJDTLVKGNAANIFKNCLKEIDSTLYKLF	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to license@isb-sib.ch).	Db	480 NLLKANVINQEHDTIKOKTOPIQOARELJDTLVKGNAANIFKNCLKEIDSTLYKLF	
DR	EMBL; U45879; AAC5032.1; -.	Qy	481 NLLKANVINQEHDTIKOKTOPIQOARELJDTLVKGNAANIFKNCLKEIDSTLYKLF	
DR	U37547; AAC50508.1; -.	Db	481 NLLKANVINQEHDTIKOKTOPIQOARELJDTLVKGNAANIFKNCLKEIDSTLYKLF	
PDB	1OBH; 20-OCT-99.	Qy	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
DR	MIM: 601721; -.	Db	600 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
DR	InterPro; IPR001370; BIR.	Qy	601 KCPICRGILRGTVRFLS 618	
DR	InterPro; IPR001841; Znf_ring.	Db	601 KCPICRGILRGTVRFLS 618	
PFam	PF00053; BIR; 3.	Qy	601 KCPICRGILRGTVRFLS 618	
DR	PFam; PF00619; CARD; 1.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
DR	PFam; PF00097; zf-C3HC4; 1.	Qy	601 KCPICRGILRGTVRFLS 618	
DR	SMART; SM00238; BIR; 3.	Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
DR	SMART; SM00114; CARD; 1.	Qy	601 KCPICRGILRGTVRFLS 618	
DR	SMART; SM00184; RING; 1.	Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
DR	PROSITE; PS01282; BIR_REPEAT; 3.	Qy	601 KCPICRGILRGTVRFLS 618	
DR	PROSITE; PS0143; BIR_REPEAT_2; 3.	Db	601 KCPICRGILRGTVRFLS 618	
DR	PROSITE; PS50209; CARD; 1.	Qy	601 KCPICRGILRGTVRFLS 618	
RW	Apoptosis; Zinc-finger; Repeat; 3D-structure.	DR	601 KCPICRGILRGTVRFLS 618	
REPEAT	46 113 BIR 1.	Qy	601 KCPICRGILRGTVRFLS 618	
REPEAT	184 250 BIR 2.	Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
FT	269 336 BIR 3.	Qy	601 KCPICRGILRGTVRFLS 618	
FT	453 539 CARD.	Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
FT	ZN_FING 571 605 RING-TYPE.	Qy	601 KCPICRGILRGTVRFLS 618	
FT	CONFLICT 157 157 S -> P (IN REF. 2).	Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
FT	CONFLICT 308 308 C -> G (IN REF. 2).	Qy	601 KCPICRGILRGTVRFLS 618	
FT	CONFLICT 414 414 Q -> L (IN REF. 2).	Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
FT	CONFLICT 514 514 L -> W (IN REF. 2).	Qy	601 KCPICRGILRGTVRFLS 618	
SQ	SEQUENCE 618 AA; 69899 MW; C1778D328063586D CRC64;	Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR	
Query	Match	RESULT 2	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Best	Local Similarity	BIR3_MOUSE	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Matches	618; Conservative	ID BIR3_MOUSE STANDARD	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	1 MHKATASQRLPGPSQNIKSIMEDESTILSDTILSWTNSNSNKQKMYDFSCELYRMSTISFPAGV 60	PRT; 612 AA.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	1 MHKATASQRLPGPSQNIKSIMEDESTILSDTILSWTNSNSNKQKMYDFSCELYRMSTISFPAGV 60	AC 062210; 008864; 01-NOV-1997 (Rel. 35, Created)	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	61 PVRSERSLARAGFYTGVNNDVKYCFCGGLMLDNWKLGDSPIOKHQKOLYPSCSFTIONLVSAS 120	DT 01-NOV-1997 (Rel. 35, last sequence update)	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	61 PVRSERSLARAGFYTGVNNDVKYCFCGGLMLDNWKLGDSPIOKHQKOLYPSCSFTIONLVSAS 120	DT 20-AUG-2001 (Rel. 40, last annotation update)	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	121 LGTSKSKNTSPRNFAHSLSPTLEHSSLFSGSYSSSLSPNPLNLSRAVEDISSRTPNSYA 180	DE BACULOVIRAL_TAP_REPEAT-CONTAINING_PROTEIN_3 (INHIBITOR_OF_APOPTOSIS	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	121 LGTSKSKNTSPRNFAHSLSPTLEHSSLFSGSYSSSLSPNPLNLSRAVEDISSRTPNSYA 180	DE PROTEIN_2) (MAP2) (MIAP-2).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	181 MSTEEARFLTYHMMWLTFLPSLSEALARAGFYIGPODRVACFACGGKLSSWEPKDAMSEH 240	GN BIRC5_OR_AP12_OR_TAP2.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	181 MSTEEARFLTYHMMWLTFLPSLSEALARAGFYIGPODRVACFACGGKLSSWEPKDAMSEH 240	OS Mus musculus (Mouse).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	241 RRHFNPCLPLENSLETURETSISNISMOthaarmrpmpyppsvvopodlasacFFYYGR 300	RC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	241 RRHFNPCLPLENSLETURETSISNISMOthaarmrpmpyppsvvopodlasacFFYYGR 300	RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	301 NDDVKFCGCCDGLRCWESGDDPWPWVHAKNPRCFLIRMKGQEFVDETOGRYPHILLEOLL 360	RT [1] NCBL-TaxID-100900;	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	301 NDDVKFCGCCDGLRCWESGDDPWPWVHAKNPRCFLIRMKGQEFVDETOGRYPHILLEOLL 360	RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins."	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	361 STSDTGEENADPPLIHFGGESESSEDAMNTVVKSALEMGRNRLVQTVQSKLTT 420	RT Cell 83:1243-1252(1995).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	361 STSDTGEENADPPLIHFGGESESSEDAMNTVVKSALEMGRNRLVQTVQSKLTT 420	RP [2]	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	421 GENKYVNDIVSALINADEKREKEKOEAREMASDDLSITRKRMALFQLTCVLPILD 480	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	421 GENKYVNDIVSALINADEKREKEKOEAREMASDDLSITRKRMALFQLTCVLPILD 480	DR MEDLINE-#6128127; PUBMED-#8558810;	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	481 NLLKANVINQEHDTIKOKTOPIQOARELJDTLVKGNAANIFKNCLKEIDSTLYKLF 540	RT Rothe M., Pan M.-G., Heuzel W.J., Ayres T.M., Goeddel D.V.;	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	481 NLLKANVINQEHDTIKOKTOPIQOARELJDTLVKGNAANIFKNCLKEIDSTLYKLF 540	RT "The TNFR2-TRAF signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins."	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR 600	RT Cell 83:1243-1252(1995).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR 600	RP SEQUENCE FROM N.A.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	RC TISSUE-Skeletal muscle.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	DR MEDLINE-#98110590; PUBMED-#9441758;	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	RA Liston P., LeFebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	RT "Genomic characterization of the mouse inhibitor of apoptosis protein 1 and 2 genes."	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	RT Genomics 46:195-205(1997).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	RT -1- FUNCTION: Apoptotic suppressor. The BIR motifs region interacts with TNF receptor associated factors 1 and 2 (TRAF1 and TRAF2) to form an heteromeric complex, which is then recruited to the tumor necrosis factor receptor 2 (TNFR2).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	RT -1- SUBCELLULAR LOCATION: Cyttoplasmic (potential).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	RT -1- TISSUE SPECIFICITY: Expressed in heart, brain, spleen, lung, liver, skeletal muscle, kidney, and testis.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	RT -1- SIMILARITY: Belongs to the TAP family.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	RT -1- SIMILARITY: Contains 3 BIR repeats.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	RT -1- SIMILARITY: Contains 1 CARD domain.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	RT -1- SIMILARITY: Contains 1 RING-TYPE ZINC FINGER.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	RT This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to license@isb-sib.ch).	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	DR EMBL; I49433; AAC42078.1; -.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	DR U88989; AAC53532.1; -.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Db	601 KCPICRGILRGTVRFLS 618	DR MGD; MGT; 1197009; BIRC3.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR
Qy	601 KCPICRGILRGTVRFLS 618	DR InterPro; IPR001315; CARD.	DR	541 VDKNNYIIPEDVSGLSLEQRRLQEEETCKVCDKEVSVWIPCGHLVCOECAASLR



			Db	601	TFLS	604
DR	InterPro; IPR001315; CARD.			1111		
DR	InterPro; IPR01841; Znf_ring.					
DR	Pfam; PF0053; BIR; 3.					
DR	Pfam; PF0053; BIR; 3.					
DR	Pfam; PF0053; BIR; 3.					
DR	SMART; SM0018; RING; 1.					
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.					
DR	PROSITE; PS50143; BIR_REPEAT_2; 3.					
DR	PROSITE; PS50209; CARD; 1.					
KW	Apoptosis; Zinc-finger; Repeat.					
FT	REPEAT	29	96	BIR 1.		
FT	REPEAT	169	235	BIR 2.		
FT	REPEAT	255	322	BIR 3.		
FT	DOMAIN	447	525	CARD.		
FT	ZNFING	557	591	RING-TYPE.		
FT	CONFLICT	18	18	N -> Y (IN REF. 4).		
FT	CONFLICT	119	119	N -> H (IN REF. 2).		
FT	CONFLICT	153	153	D -> E (IN REF. 2).		
FT	CONFLICT	163	163	H -> P (IN REF. 2).		
FT	CONFLICT	165	165	A -> P (IN REF. 2).		
FT	CONFLICT	191	191	K -> R (IN REF. 2).		
FT	CONFICT	364	364	F -> L (IN REF. 2).		
FT	SEQUENCE	604	AA:	68371 MW; 8581A00BA9ABA7 CRC64;		
Query Match			Score	2353;	DB 1;	Length 604;
Best Local Similarity			71.8%			
Matches	440;	Conservative	71;	Mismatches	87;	Indels 6; Gaps 5;
Oy	20 SIMEDSTLSDWNTNS NKOKKYYDFSCELYRMSYSTFPAGVPUERSLARAGFYTTGVN	78				
Db	2 NIVENTSILNLNMKSANTEELKYLDSLCELYRMSTYRPAVGVPERSLARAGFYTTGVN	61				
Oy	79 DKVKCPCGGLMDNWKGDSPIQKAROLYPSFCFTONLVAA-SLGSTSKMSP--MRNSP	135				
Db	62 DKVKCPCGGLMDNWKGDSPIEKKKLKFSCRFVQSLNSVNNLRTSQPTFPSSVNTS-	120				
Oy	136 AHSLSTLEHNSLFSGSYSSSPNPILNSRAVEDDSSRNPYSTAMSTAEAREFTYHMNP	195				
Db	121 THSLLPGTENSGYFRGYSNSPNPSNPNSRANQDFSLALMRSYHCAANNENARLTFOTNP	180				
Oy	196 LTPLPSSELARAGFVYIGPDRYAPACGGKLNSWPKDAMSRHRRHPPNCPIEPLSL-	254				
Db	181 LTPLSPDLAKAFYIIGPDRVACFACGSKLNSWPKDAMSHRLRHPPKCPRENQO	240				
Oy	255 ETFLPSSELARAGFVYIGPDRYAPACGGKLNSWPKDAMSRHRRHPPNCPIEPLSL-	214				
Db	241 DTSPRYTVNSLNSMOTHAARPKUFFNPSSVLPVNEPOLASAGFYVGENSDVKFCFDGLR	300				
Oy	315 CWESGGDPWPWHEKAWPWRPCEFLRIMQGQEVFDETOGRYPHILEQQLSTSPTGRENADPP	374				
Db	301 CWESGGDPWPWHEKAWPWRPCEFLRIMQGQEVFDETOGRYPHILEQQLSTSPTGRENADPP	360				
Oy	375 ITHFGGESESSEDAYMVNTPVKSALEMGNRDIYKOTVOSKINTTGENVKTVNDIVSAL	434				
Db	361 ITHFEGEDHSIDAIMMNTPVINAEMVGMFSRSVLYKOTVORKVILATGENYRLVNDVLQ	420				
Oy	435 LNADKEEKEKQKEMMASDDSLIRKRNMAFQHLTCVITPLDLSLTAGTNEQED	494				
Db	421 LNADETREERERATEEKESNDLLIRKRNMAFQHLTCVITPLDLSLTAGTNEQED	480				
Oy	495 IKKQKTOIQPLQARELDTILVKGNAANIFRNCKLKEIDSTLYKKLFDKNKYIPTEDVS	554				
Db	481 VIKQKQTQSLQARELDTILVKGNAANIFRNCKLKEIDSTLYKKLFDKNKYIPTEDVS	540				
Oy	555 GLSLEFOLRRIQERERICKVQMDKEVSVWFLPGHILWCQBCAPSURKCPICRGITKGT	614				
Db	541 DLPEVEQLRQLQERTCKVQMDKEVSVIWFPGHILWCQBCAPSURKCPICRGITKGT	600				
Oy	615 TFLS 618					
Query Match			Score	2233.5;	DB 1;	Length 611;
Best Local Similarity			69.2%			
Matches	424;	Conservative	77;	Mismatches	95;	Indels 17; Gaps 8;
Oy	20 SIMEDSTLSDWNTNSNKQ--KMKYDFSCELYRMSYSTFPAGVPUERSLARAGFYTTGVN	77				

Db	2 NINDSSPLASVMKONAHCGLKDFSCELYRMSTFSTFPVNVPVSRLLARAGFYFTGV	61	Cc	-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
Oy	78 NDVKVKPCCGIMLDWIKLGSPIOKHKQLYPSCSFIQIYSA-SIG-ST-----SKN	127	Cc	....
Db	62 QDKVKCSCGIVLDNQPGONAMEMHKQYPSFVQNLSLNLGJLSTSFAFLSPVLSA	121	Cc	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
Oy	128 TSPMRNSFAHSLSPLEHSSLFSSYSSLSPNPLNSRAVEDTSSSRNPYSAMSTEAR	187	Cc	....
Db	122 LSPSLRSM--TLSPSREQVSYFSSFSFRDPVTPTRAEDLSHLRSKLQPSMSTEAR	179	Cc	....
Oy	188 FITYHHMPLFLPSELARAGFYFTGPDRVACFGCKLSNPKDAMSHRHRRHPPNC	247	Cc	....
Db	180 LRTSHAMPLMOLWPAEKAGLDDGTAQKVAQNCVGKLSNPKDAMSHRHRRHPPNC	239	Dr	DR EMBL; U08908; AAC53531.1; -.
Oy	248 PFLLENSL-ETLRFSISNLNSMOTHARMRTPMFYWSVSVQPEOOLASAGFYVGRNDYKC	306	Dr	DR MGD; MGI:1197007; Birc2.
Db	240 PFEVNLMDRQDPSPFNFNSNVNTQTHBARYKFINWTRIPVQPEALADAGFYVGRNDYKC	299	Dr	DR InterPro; IPR001370; BIR.
Oy	307 FCCDGGLRCWESGDDPWEHAKWPFCEFLRMMQGEFDETQGRYPHLL-BOLUSTSDT	365	Dr	DR InterPro; IPR01315; CARD.
Db	300 FCCDGGLRCWESGDDPWEHAKWPFCEFLRMMQGEFDETQGRYPHLL-BOLUSTSDT	359	Dr	DR InterPro; IPR001841; Znf_fing.
Oy	366 TGEENADPPIHFGESESSDAVNMNTPVKSALEMFKNRDVKQYQVOSKILTGENYK	425	Dr	DR Pfam; PF00653; BIR; 3.
Db	360 PVDENMD-PIHPEGPSBESDAIMNTPVKALEMFSRRLIKQTWOSKILATEBYN	418	Dr	DR Pfam; PF00097; Zn-C3Hc4; 1.
Oy	426 TUNDIVSALLNAEDEKEEKEQAEEMASDLSLIRKRNMLALEQQLTCVPIIDNLJKA	485	Dr	DR SMART; SM00238; BIR; 3.
Db	419 TVNDLVESELLTAEDEKEEKEQEEFEEVASDSLILRKRNMLAFRLTSVPLISLA	478	Dr	DR SMART; SM00114; CARD; 1.
Oy	486 NWINKQEHDTIKQKTOIPLQARELIDTLVKGNAANIFKNCKIEIDSTLYKNLFDKNM	545	Dr	DR SMART; SM00184; RING; 1.
Db	479 KVITELHDVHQTKTQTPSQARELIDTVLKGNAASIFRNCKIKDFEPVLYKDFEVKSM	538	Dr	DR PROSITE; PS0143; BIR_REPEAT_2; 3.
Oy	546 KVIPTEDVSGISLQEORRQFERTCKVCMDEKSVVFLPCGHILWVQECAPSLRKCPIC	605	Dr	DR PROSITE; PS0209; CARD; 1.
Db	539 KVIPTEDVSGISLQEORRQFERTCKVCMDEKSVVFLPCGHILWVQECAPSLRKCPIC	598	Dr	DR Apoptosis; Zinc-finger; Repeat.
Oy	606 RGTIKGTVRTEFLS	618	Ft	FT REPEAT 27 94 BIR 1.
Db	599 RGTIKGTVRTEFLS	611	Ft	FT REPEAT 167 233 BIR 2.
RESULT	5	Matches	Ft	FT REPEAT 253 320 BIR 3.
BIR2_MOUSE	STANDARD;	PRT;	Ft	FT DOMAIN 444 512 CARD.
ID	BIR2_MOUSE		ZN_FING	ZN_FING 553 587 RING-TYPE
AC	00863;		SEQUENCE	SEQUENCE 600 AA; 67198 MW; ADP73E6649317DI CRC64;
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	BAULOTRIAL IAP REPEAT-CONTAINING PROTEIN 2 (INHIBITOR OF APOPTOSIS PROTEIN 1) (MIAP1) (MIAP-1).			
GN	BIRC2 OR APL1 OR IAP1.			
OS	MUS musculus (Mouse); OC Ekarvycia; Metacara; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. OX NCBI_TAXID=10090; RN {1}			
RP	SEQUENCE FROM N_A.			
RN	TISSUE-skeletal muscle;			
RX	Medline:9810390; PubMed:9411758; Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.; "Genomic characterisation of the mouse inhibitor of apoptosis protein 1 and 2 genes.", Genomics 46:495-503(1997).			
RX	"FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2), TO FORM AN HETEROmeric COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL). SIMILARITY: BELONGS TO THE IAP FAMILY. SIMILARITY: CONTAINS 3 BIR REPEATS. SIMILARITY: CONTAINS 1 CARD DOMAIN.			



CC	-1 TISSUE SPECIFICITY: UBIQUITOUS, EXCEPT PERIPHERAL BLOOD	Db	426 -----:   -----   -----KEI-----	435
CC	LEUKOCYTES.			
CC	-1 SIMILARITY: BELONGS TO THE IAP FAMILY.			
CC	-1 SIMILARITY: CONTAINS 3 BIR REPEATS.			
CC	-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch">http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch</a> ).			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: U45880; AAC50373.1; -	ID	BIR4_MOUSE STANDARD; PRT; 496 AA.	
DR	EMBL: U32974; AAC50318.1; -	AC	Q60989; 008865; -	
DR	EMBL: AL121601; CAB95312.1; -	DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DR	MIM: 30079; -	DT	01-NOV-1997 (Rel. 35, Last annotation update)	
DR	InterPro: IPR001370; BIR.	DT	20-AUG-2001 (Rel. 40, Last annotation update)	
DR	InterPro: IPR001841; Znf_ring.	DE	BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS PROTEIN 3) (X-LINKED INHIBITOR OF APOPTOSIS PROTEIN) (X-LINKED IAP)	
DR	Pfam: PF00653; BIR; 3.	DE	(IAP HOMOLOG A) (MAP3) (MAP-3).	
DR	Pfam: PF00097; zf-C3HC4; 1.	GN	BIRC4 OR API3 OR XIAP OR AIPA OR MIHA.	
DR	SMART: SM00238; BIR; 3.	OS	MUS MUSCULUS (Mouse).	
DR	SMART: SM00184; RING; 1.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
DR	PROSITE; PS5013; BIR_REPEAT; 3.	OX	NCBI_TAXID=10909;	
KW	Apoptosis; Zinc-finger; Repeat; Thiol protease inhibitor.	RN	[1]	
FT	REPEAT 26 93	RP	SEQUENCE FROM N.A.	
FT	REPEAT 163 230	RX	RENAME=57BL/6 X CBA: TISSUE=Liver;	
FT	REPEAT 230 26	RA	MEDLINE=9620843; Pubmed=864354;	
FT	REPEAT 162 162	RA	Ouren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;	
FT	CONFLICT 423 423	RT	"Cloning and expression of apoptosis inhibitor protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors";	
SQ	SEQUENCE 497 AA; 56684 MW; 9D394C16D45EB635 CRC64;	RT	Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).	
Query Match	27.8%; Score 911; DB 1; Length 497;	RN	[2]	
Best Local Similarity	33.8%; Pred. No. 6e-54;	RP	SEQUENCE FROM N.A.	
Matches	205; Conservative 89; Mismatches 163; Indels 150; Gaps 14;	RA	Farahani R., Leefevre C., Korneluk R.G., Mackenzie A.E.; Submitted (JUN-1997) to the EMBL/Genbank/DDBJ databases.	
Qy	35 NKQKMKYDFSFCELYRMYSTSTFPAGPVPSRSALARAGFYVTGVNDVKPCFCGIMLDNNK 94	RL	-1 FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND CASPASE-7 (BY SIMILARITY).	
Db	18 NKE---EFVEFRNURKTFANFPGSPSPVSASTLARAGFLYGEQEDTVRFSCHAVIDRQQ 74	CC	-1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).	
Qy	95 LGDSPIQKHOLYPSCSFIONVLASIGSTSNTSPMRNF-AHSLSPLEHSSLFSGSY 153	CC	-1 SIMILARITY: BELONGS TO THE IAP FAMILY.	
Db	75 YGDSAVGRHRKVSPNCRFINGFLYLENSTATOSTNSQGKYKVENYLGSRDHFALDRPS- 133	CC	-1 SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	
Qy	154 SSLSPNPLNSRAVEDTSSSRPNPYSAMSTEARLTYHMP-LTFLSSELARAGFYI 212	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch">http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch</a> ).	
Db	134 ETHADYLRLRTGQVDISDT-TPYRNPAMYSEARLKSQFWNPDAHLTPRELASAGLYT 192	CC	or send an email to license@isb-sib.ch).	
Qy	213 GPGDRVACFAGGGKLSNWEPKDDAMSEHRRHPPNGPFL-----EN 252	CC	DR: U36842; AAC52594.1; -	
Db	193 GIGDQVQFCGGKLKNWECDRMANSEHRRHPPNGPFL-----EN 252	DR	DR: U36890; AAB8376.1; -	
Qy	253 SLETLRPSISNM-MOHAARMRTFMWPSVPPQPEBOLASAGFYVGRNDVKPCDCG 312	DR	MGD: MGI-107572; Birc4.	
Db	307 LTDWKPSEDPWEHQAKWPKYLGKLLQKGQYINNT--HLTHSLRECLVTT----- 359	DR	InterPro: IPR001370; BIR.	
Qy	372 DPPPIIHRGPGESSESSEDAVMANTPPVKSALLENGFNRDLVKVQSVSILTGENYVTDIV 431	DR	InterPro: IPR001841; Znf_ring.	
Db	313 LRCWEGGDDPWPHEAHKWPCEFLIRMKGCPYDITOGYPHILQFQ-LUSTSDPGEENA 371	DR	Pfam: PF00653; BIR; 3.	
Qy	307 LTDWKPSEDPWEHQAKWPKYLGKLLQKGQYINNT--HLTHSLRECLVTT----- 359	DR	Pfam: PF00097; zf-C3HC4; 1.	
Db	372 DPPPIIHRGPGESSESSEDAVMANTPPVKSALLENGFNRDLVKVQSVSILTGENYVTDIV 431	DR	SMART: SM00184; RING; 1.	
Db	360 -----PSLTTRIDTIFONPMPQEAIRMGFSFRDKIKIMERIQISGSNSYKSLLEV 411	DR	PROSITE; PS01282; BIR_REPEAT_1; 3.	
FT	REPEAT 26 93	DR	PROSITE; PS01043; BIR_REPEAT_2; 3.	
FT	REPEAT 163 230	KW	Apoptosis; Zinc-finger; Repeat.	
FT	REPEAT 264 329	FT	REPEAT 163 230	
FT	ZN_FING 449 483	FT	ZN_FING 449 483	
FT	CONFICT 208 208	FT	RING-TYPE.	
FT	CONFICT 317 317	FT	E->K (IN REF. 2).	
Qy	492 EHDIIKQTKPLQARBLIDTILVKGNAANIFKNCLKEIDSTYRNLFVDKNRYVPT 551	FT	E->D (IN REF. 2).	



**Db** 398 TSGSNLISLEVLLADLVSQAKDMSQDE----- 424  
**Qy** 479 LDNLKANVINKQHQHDLIKQTOPLQARELIPITLVKGNAANIFKNCLKEIDSTLYKN 538  
**Db** 425 -----SSPSLSQ----- 431  
**Qy** 539 LFVVKNMVKIPTEDVGSLSLEQFARRLQFERTCKVCMQEVSVWFIPOGHLVVQECAPS 598  
**Db** 432 -----KDISTEQQRRLQEEKLCKICMDRNIAIWFPQGHLYCCKQCRAE 476  
**Qy** 599 LRKGPICRGIIKGTVRTEFS 618  
**Db** 477 VDKCPMCCIVITFFQKIFMS 496

**RESULT** 10

**IAP2-DROME** STANDARD: PRT; 498 AA.

**ID** IAP2-DROME AC Q24307; Q24177; Q24115; Q24149; Q9V7G1;  
**DT** 01-NOV-1997 (Rel. 35, Created)  
**DT** 01-NOV-1997 (Rel. 35, Last sequence update)  
**DT** 20-AUG-2001 (Rel. 40, last annotation update)

**DE** APOPTOSIS 2 INHIBITOR (INHIBITOR OF APOPTOSIS 2) (DIAP2) (DIAP) (IAP HOMOLOG 5) (IAP-LIKE PROTEIN) (DILP).  
**DE** IAP2 OR ILP OR DIHA OR CG8293.  
**OS** Drosophila melanogaster (Fruit fly).  
**OC** Eukaryota; Arthropoda; Tracheata; Hexapoda; Insecta;  
**OC** Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.  
**OX** NCBI\_TaxID=7277;  
**RN** [1]  
**RP** SEQUENCE FROM N.A.  
**RC** TISSUE-EYE imaginal disk;  
**RX** MEDLINE-#6128128; PUBMED-8548811;  
**RA** Hay B.A., Wassarman D.A., Rubin G.M.;  
**RT** "Drosophila homologs of baculovirus inhibitor of apoptosis proteins function to block cell death.";  
**RL** Cell 83:1253-1262(1995).  
**RN** [2]  
**SEQUENCE FROM N.A.**  
**RC** TISSUE-Embryo;  
**RX** MEDLINE-#6149349; PUBMED-8552191;  
**RA** Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertoff-Horvat G., Farahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;  
**RT** "Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes";  
**RL** Nature 379:349-353(1996).  
**RN** [3]  
**RP** SEQUENCE FROM N.A.  
**RC** STRAIN-CANTON-S;  
**RX** MEDLINE-#6256286; PUBMED-8654366;  
**RA** Duckett C.S., Nava V.E., Gedrich R.W., Clem R.J., van Dongen J.L., Gilfillan M.C., Shieh S.H., Hardwick J.M., Thompson C.B.;  
**RT** "A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors.";  
**RL** EMBO J. 15:2685-2694(1996).  
**RN** [4]  
**SEQUENCE FROM N.A.**  
**RC** STRAIN-CANTON-S;  
**RA** Ross J.L.;  
**RL** Thesis (1991), Vanderbilt University / Nashville, U.S.A.  
**RN** [5]  
**SEQUENCE FROM N.A.**  
**RC** STRAIN-BERKELEY;  
**RX** MEDLINE-#20196006; PubMed-1071132;  
**RA** Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hostins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Milos L.G., Abrial J.F., Abyzov A., An H.-J., Andrews P., Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottner P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Deicher A., Deng Z., Mays A.D., Dew T., Dietz S.M., Dodson K., Douc E., Dowens M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hock C.J., Houston D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosheff A., Mount S.M., Moy M., Murphy B., Murphy L., Murray D.M., Nelson D.R., Nelson K., Nixon K., Nusslein-Davidson D.R., Paciello J.M., Nelson D.R., Nelson D.R., Pollard J., Puri V., Reissig M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sider-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svarskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng D., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
**RT** "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).  
**RN** [6]  
**RP** SEQUENCE OF 17-498 FROM N.A.  
**RC** TISSUE-larva;  
**RX** MEDLINE-#6208943; PubMed-8643514;  
**RA** Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.J.;  
**RT** "Cloning and expression of apoptosis inhibitory protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";  
**RT** Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).  
**CC** -!- FUNCTION: APOPTOTIC SUPPRESSOR. OVEREXPRESSION SUPPRESSES RPR AND HID-DEPENDENT CELL DEATH IN THE EYE.  
**CC** -!- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS THROUGHOUT DEVELOPMENT. BELONGS TO THE IAP FAMILY.  
**CC** -!- SIMILARITY: CONTAINS 3 BIR REPEATS.  
**CC** -!- SIMILARITY: CONTAINS 1 RING-TIE ZINC FINGER.  
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**CC** -----  
**DR** EMBL; I4941; AAC41610; 1;  
**DR** EMBL; U45881; AAC46988; 1;  
**DR** EMBL; U32373; AAC47155; 1;  
**DR** EMBL; M66581; -; NOT\_ANNOTATED\_CDS.  
**DR** EMBL; AR003808; RAF58095; 1; -.  
**DR** EMBL; U38809; AAC08398; 1;  
**DR** FlyBase; FBgn0015247; Iap2.  
**DR** InterPro; IPR001370; BIR.  
**DR** InterPro; IPR001841; Znf\_ring.  
**DR** Pfam; PF00653; BIR; 3.  
**DR** SMART; SM00238; BIR; 3.  
**DR** SMART; SM00184; RING; 1.  
**DR** SMART; SM01282; BIR\_REPEAT; 1; 3.  
**DR** PROSITE; PS50143; BIR\_REPEAT\_2; 3.  
**KW** Apoptosis; Zinc-finger; Repeat.  
**FT** REPEAT 9 76 BIR 1.  
**REPEAT** 9 179 BIR 2.

FT	REPEAT	212	279	BIR 3.
FT	ZN FING	451	485	RING-TYPE.
FT	CONFICT	5	5	G -> V (IN REF. 2).
FT	CONFICT	40	40	N -> K (IN REF. 2).
FT	CONFICT	64	65	ER -> AG (IN REF. 3).
FT	CONFICT	94	94	E -> K (IN REF. 1).
FT	CONFICT	282	282	A -> D (IN REF. 6).
FT	CONFICT	286	286	A -> S (IN REF. 3).
FT	CONFICT	302	302	P -> Q (IN REF. 2 AND 5).
FT	CONFICT	303	303	P -> T (IN REF. 6).
FT	CONFICT	327	327	A -> T (IN REF. 2).
FT	SEQUENCE	498	AA:	ALEREPR -> DIRACSR (IN REF. 3).
SQ	SEQUENCE	498	AA:	54506 MW; 66RC36DA6ED24AD6 CRC64;
Query Match	Best Local Similarity	22.7%	Score	744/5; DB 1; Length 498;
Matches	Local Similarity	30.8%	Pred. No.	9e-43; Mismatches 206; Indels 117; Gaps 16;
Qy	46	ELYRMSTYSTPAGPVNSERSLARAGFYTGVNDVKVQFCGMLMDNNKKLGDSPIKHKQ	105	CC
Db	9	ESVRULATEGKWLPLAPVPSAEDBLVANGFEATGNWLEAECHFCHYRDRMEYGDQAERR	68	CC
Qy	106	LYPGCSFIQNLVSAISLGSITSKNTSPMRNSFAHSLSPTLEHSSLFSGSYSSLNPNLNSRA	165	CC
Qy	166	VEDISSLSSRNTPYSYMSTSERFLTYHMPLTEFLSPSELARAGFYYIGPDRYACFACGG	225	CC
Db	69	SSPICSMV--LAPNHCGNWRP-----SSESNEGNS--	97	CC
Qy	226	KLSNWEKPDDAMSGBRRHFPNCPLE-----NSLETARPSISNLSMQTH--AA	271	CC
Db	155	VIAKWKEKNDAFEEEHKRFPOCPVRQVMGLIEFATGKNELEGLIOPPTLPLRPKYACVDA	214	CC
Qy	272	RMRFMWVWSSSVPQP-EQLASAGFYVVERNDYKCFCCDGLRCWESCDPWPHEAKWF	330	CC
Db	215	RLRFFTDWMS-NTOPALAQAGLYYQKGQYRCFHICNIGRSWQREDPWEHAKWS	273	CC
Qy	331	PRCEFLIRMKQGEFVDELOGRYPHQLQESTSDTGEENADPPIIHFGPGESSEDAM	390	CC
Db	274	PKCQVLLAAGPAVSEVLA-----TTAANASSPAT-APAPIQLADYL	317	CC
Qy	391	MNTPVVKSALEMGNFRDLVYKQTVOSKILTGENTYKVNDIVSALLNAEDEKREEEKQKA	450	DR
Db	318	DEAP-AKEALALGTDGVVNRNAIKORKLSSGCAFSSTLDLHDIFDDAGAALEVRREP	376	DR
Qy	451	EEMASDDLSLIRKRMALQOLTCVLPILNDLKLKANVINKQEHQIJKTKOIPU-QRE	508	DR
Db	377	EPSA----PEIPEQCATTSKRAASVYPIVADS-----IPAKPOKE	412	DR
Qy	509	LIDITLVKGNAANIFNKNCNLKEIDSTLYKLNFVDKNMKYIPTEDVSGSLEEQRQOE	568	DR
Db	413	-----AVANTISK-----TDEIORMSWAPPNGNLSEEEENROLDA	448	DR
Qy	569	RTCKVMDKEEVSVVFIPCGHLVWQECAPSRLRKCPICRCIGTKGVTRTL	618	DR
Db	449	RICKVCLDDEVGVVFLPCGHLATCNOQCAPSVAANCMPMCRADIKGFRVFTLS	498	DR
RESULT	11			
IAP3_NPVOB	STANDARD;	PRT;	268 AA.	
ID	IAP3_NPVOB			
AC	P4137;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-Nov-1995 (Rel. 32, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	APOPTOSIS INHIBITOR 3 (IAP-3).			
DE	IAP3 OR IAP.			
OS	Orgyia pseudotsugata multicapsid Polyhedrosis virus (OpMVNPV).			
OC	Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.			
OC	NCBI_TaxId:1666293;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-94187094; PubMed-8139034;			
RA	Birnbaum M.J., Clem R.J., Miller L.K.;			
RT	"An apoptosis-inhibiting gene from a nuclear polyhedrosis virus encoding a polypeptide with a Cys/His sequence motifs";			
RT	J. Virol. 68:2521-2528(1994).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE-9721300; PubMed-9126251;			
RA	Antens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.;"The sequence of the <i>Orgyia pseudotsugata</i> multinucleocapsid nuclear polyhedrosis virus genome.", Virology 229:381-399(1997).			
RT	-!!- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY PREVENTING VIRAL STIMULATION OF APOPTOSIS.			
CC	-!!- SIMILARITY: CONTAINS 2 BIR REPEATS.			
CC	-!!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
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DR	EMBL; I22564; AAC802610; 1;			
DR	EMBL; U75930; AAC59034; 1;			
DR	InterPro; IPR01370; BIR.			
DR	InterPro; IPR001841; Znf_fing.			
PFam	PF00653; BIR; 2;			
PFam	PF0097; zf_C3HC4; 1.			
SMART	SM0038; BIR; 2;			
SMART	SM0084; RING; 1.			
DR	DR PROSITE; PS01282; BIR_REPEAT_1; 2.			
DR	DR PROSITE; PS05143; BIR_REPEAT_2; 2.			
KW	Apoptosis; Zinc-finger; Repeat.			
FT	REPEAT 18 84 BIR 1.			
FT	REPEAT 111 178 BIR 2.			
FT	ZN FING 221 255 RING-TYPE.			
SO	SEQUENCE 268 AA: 30076 MW; DF89175FDE05A708 CRC64;			
Query Match	Best Local Similarity	15.7%	Score	513; DB 1; Length 268;
Matches	Local Similarity	24.1%	Pred. No.	1.3e-27; Mismatches 86; Indels 200; Gaps 107; Conservative
Qy	181	MSTEARFLTYHMLPLTFLSPSLARAGFYYIGPDRYACFACGGKL-SNWEPRKDAMSEH	240	Qy
Db	15	MKNAKAARGTYTNWVQFLEPSKMAASGFYIPLGRDVEURCARCKVETNWVGRGDDETDH	74	Qy
Qy	241	RRIHPNCFEPLENSE-----TRLSISISMOTAHMARTTMWPPSSVYQPOQAS	292	Qy
Db	75	KRMAPQPIFVRNNAHDTPHRDAPPRAAHPOYATAARLTFIAEWAHRPGLQKQRPBEEAE	134	Db
Qy	293	AGYYVGRNDYKVFCCDGGLRWESDDPWPTEHAKWPFREFLIRKGQSERVDEIGRY	352	Qy
Db	135	AGFFYTGODKTKRCFCDCGGLKWDPEPDAPWQHARWYDRCYVLLVKGRDFVOR	189	Db
Qy	353	PHLEOLIISTSDTIGEMENADPPIHFGRGESSEDAMVNTPVVKSALEMGNFRDLVQKT	412	Qy
Db	190	-----VTEACVVR-----	198	Db
Qy	413	VOSKILTGENTYKVNDIVSALLNAEDEKREEEKQAEAMASDDLSLIRKRMALFOOL	472	Qy
Db	199	DADPHEPTPVAE-----	214	Db
Qy	473	TCVLPILDNLKANVINKQEHDTIKQHQIPLQARELIDTILVKGNAAANIFNKCLREID	532	Qy
Db	215	-----	214	Db

QY 533 STLYKNLFVDKNNMKVPIPEDVSGSLSLQQERTCKVCMKDEVSVMFIPGHLVWC 592  
 FT REPEAT 278 345 BIR 3.  
 Db 215 ..... VADDRLCKICLGAEKTVCFPGHVVAC 242 K -> R (IN REF. 1).  
 DR PROSTE; PS01482; BIR\_REPEAT\_1; 2.  
 DR PROSTE; PS01482; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 DR MGI:1298220; Bircle.  
 DR Interpro; IPR001370; BIR.  
 DR Pfam; PF00653; BIR; 3.  
 DR SMART; SM00238; BIR; 3.  
 DR EMBL; AF131205; AD56760; 1; -.  
 DR EMBL; U66326; AAC52974; 1; -.  
 DR REPEAT 159 227 BIR 2.

RESULT 12  
 BIRE\_MOUSE STANDARD; PRT; 1403 AA.  
 AC 09R016; 09R029; P81703; 009122; 009121;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

BIRE\_MOUSE INHIBITOR PROTEIN 5 (NEURONAL APOPTOSIS INHIBITOR PROTEIN 5).  
 BIRCIE OR NATIVE NAIPI-RS3.  
 OS Mus musculus (Mouse).  
 OC Birkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 NCBI\_TAXID=10090;

RN [1] SEQUENCE FROM N.A.  
 RP MEDLINE-9416767; PubMed-10501978;  
 RX RA Huang S., Scharf J.M., Grawley J.D., Endrizzi M.G., Dietrich W.F.;  
 RT "The mouse Naip gene cluster on Chromosome 13 encodes several distinct functional transcripts";  
 RL Mamm. Genome 10:1032-1035(1999).

RN [2] SEQUENCE FROM N.A.  
 RP STRAIN=129/SV;  
 RX MEDLINE-9416764; PubMed-10486205;  
 RA Endrizzi M., Huang S., Scharf J.M., Kelter A.R., Wirth B.,  
 RT "Comparative sequence analysis of the mouse and human Lgn1/SMA interval";  
 RL Genomics 60:137-151(1999).

RN [3] SEQUENCE OF 82-168 FROM N.A.  
 RP STRAIN=129/SV;  
 RX MEDLINE-97131520; PubMed-8915718;  
 RA Scharf J.M., Damron D., Frisella A., Bruno S., Beigs A.H.,  
 RA Kunkel L.M., Dietrich W.F.;  
 RT "The mouse region synteny for human spinal muscular atrophy lies within the Lgn1 critical interval and contains multiple copies of Naip exon 5";  
 RL Genomics 38:405-411(1996).

CC -- FUNCTIONS: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF SIGNALS.

CC -- SIMILARITY: CONTAINS 3 BIR REPEATS.

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CC EMBL; AF1315492; AD56764; 1; -.  
 CC EMBL; U66326; AAC52974; 1; -.  
 CC MGD; MGI:1298220; Bircle.  
 CC Interpro; IPR001370; BIR.  
 CC Pfam; PF00653; BIR; 3.

DR SMART; SM00238; BIR; 3.  
 DR PROSTE; PS01482; BIR\_REPEAT\_1; 2.  
 DR PROSTE; PS01482; BIR\_REPEAT\_2; 3.  
 KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 DR REPEAT 159 227 BIR 2.

FT REPEAT 278 345 BIR 3.  
 FT CONFLICT 92 92 K -> R (IN REF. 1).  
 FT CONFLICT 144 144 S -> R (IN REF. 1).  
 FT CONFLICT 242 242 S -> G (IN REF. 2).  
 FT CONFLICT 472 472 T -> A (IN REF. 2).  
 FT CONFLICT 516 516 A -> D (IN REF. 2).  
 FT CONFLICT 521 521 A -> T (IN REF. 2).  
 FT CONFLICT 533 533 V -> A (IN REF. 2).  
 FT CONFLICT 538 538 S -> T (IN REF. 2).  
 FT CONFLICT 1092 1092 E -> D (IN REF. 2).  
 FT CONFLICT 1129 1129 H -> L (IN REF. 2).  
 FT CONFLICT 1137 1137 R -> Q (IN REF. 2).  
 FT CONFLICT 1242 1242 V -> I (IN REF. 2).  
 FT CONFLICT 1276 1276 D -> N (IN REF. 2).  
 SQ 1403 AA; 159695 MW; B27f645043BCE42 CRC64;

Query Match 15 48; Score 506; DB 1; Length 1403;  
 Best Local Similarity 27.3%; Pred. No. 3; ge-26; Gaps 27;  
 Matches 175; Conservative 73; Mismatches 216; Indels 176; Gaps 27;

OY 14 SYONIKSIMEDSTILSDWNTNSNKRKMVKDFSCF---LYRMSTYSTFFAGVPUERS 66  
 Db 31 AFOVAKSQEEEE-----HKERMKMKGFNSMRSEKRIKTFENYDTRFSWTP---QE 80

OY 67 LARAGYYTSNDKVCFCCGMLDNWKDGDSPIOKHOLYSCFTIONLVASLGSTS 126  
 Db 81 MAAGFTYHGKLGVQCFCSSLIFGLNSLRKPLIERKKLRECEFLQ--GKDWNIGK 137

OY 127 NTSPMNSFAISLSTPLENNSLSSGSYKSLSPRLNRAVEDISSPNTNPYSYANSTEEA 186  
 Db 138 YDIRVK-----SPEKM-----LGGKARY--HEEEA 161

OY 187 RELTYHWMPFL--LPSELALARCFYVTPGPWDVACFAGGKLNSNMPKDDAMSEHRRF 244  
 Db 162 RULESFEDWPYAHGTSPPRVSAAFWFNGKDRPTQCSFGGSLGNHREGDDPPWKEAWF 221

OY 245 PNCPFLEN- SLETLRFSTSNSLNSMOTHAA-----R 272

OY 222 PRKFELQSKSSEEIAQYIQSYYEGFVHYGEHFVKSWRRELPMVSAYCNDSVFANEELR 281

OY 273 MRTFMWPPSSVPPQDPLASAGAFYVGRNRDDVWCFCCCGGLRQEWESDDPPWHEAKWPR 332

Db 282 KDMFKWNPQESPPGVYEAFLVRAFGFPYTKKDIYRCFSCGGCLKWAEDDPWEDHIFKFP 341

OY 333 CEFFLIRMKGQ-EFVDEIQGRPHLQLSTSDTGREEN-ADPITH----- 377

Db 342 CYFLQTLKSSSEEVIPLOSOY---ALPATEITRESHGDAAHVSTVULGRSEAQN 396

OY 378 FPGGESEDAA-----WMIMTPVWKSAL-----EMGFNRDLVQWQSKLTT 420

Db 397 FOEARSLSEQRLDNYTAKTERHMNLPEVCSSLGLDHLSCDVSIISKHSIOPVQ-BALTI 455

OY 421 GENKYKVNIDYVALLNAEKKREEK-- EKQAREMASDLSLTKRMRMAFFPOLICVLP 477

Db 456 PEVFNSLNVMC---VEGETGSKTFELKRAFLWASGCCPLYRFOLVYFLSUSITP 511

OY 478 ILDNLKANVYINKQHQBDIJKKTQIPLQARELDTILVKGNAANTKNCI-KEIDSTLY 536

Db 512 --DOGL-ANITCAQ-----LLGAGCISEV--CLASS1OQLQH 544

OY 537 KNLFVDKNNMKVPIPEDVSGL-SLEFQRRLQEE-- RTC 571

Db 545 QVFL-----LDDYSGLASLPQALHTLTKNYLRSRC 576

RESULT 13  
 BIRE\_MOUSE STANDARD; PRT; 1403 AA.  
 ID BIRE\_MOUSE  
 AC Q9JTB6; P81704; 009122; 009121;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE BACULOVIRAL LAP REPEAT-CONTAINING PROTEIN 1F (NEURONAL APOPTOSIS  
 DE INHIBITORY PROTEIN 6).  
 GN BIRC1P OR NAIP6 OR NAIP-R54.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus;  
 OX NCBI\_TAXID=10990;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20414747; PubMed=10958627;  
 RA Endrizzi, M.G.; Hadinoto, V.; Grawney, J.D.; Miller, W.; Dietrich, W.F.;  
 RL "Genomic sequence analysis of the mouse Naip gene array.";  
 RL Genome Res. 10:1095-1102(2000).  
 RN [2]  
 RP SEQUENCE OF 82-168 FROM N.A.  
 RX MEDLINE=97131320; PubMed=8925718;  
 RA Scharf, J.M.; Damron, D.; Friesella, A.; Bruno, S.; Beggs, A.H.;  
 RA Kunkel, L.M.; Dietrich, W.F.;  
 RT "The mouse region syntetic for human spinal muscular atrophy lies  
 within the IgM1 critical interval and contains multiple copies of Naip  
 exon 5.";  
 RL Genomics. 38:405-417(1996).  
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
 CC SIGNALS.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC .....  
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 CC .....  
 DR EMBL: AF242431; AAF82751.1; -.  
 DR EMBL: 06527; AAC53975.1; -.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM00238; BIR; 3.  
 DR PROSITE: PS01282; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS05043; BIR\_REPEAT\_2; 3.  
 DR KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 FT REPEAT 159 227 BIR 2.  
 FT REPEAT 278 345 BIR 3.  
 SQ SEQUENCE 1403 AA; 159823 MW; 9d4912503358C4E9 CRC64;

RESULT 14  
 BIRG\_MOUSE STANDARD; PRY; 1402 AA.  
 ID BIRG\_MOUSE STANDARD; PRY; 1402 AA.  
 AC Q9J133;  
 DT 20-AUG-2001 (Rel. 40, created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20414747; PubMed=10958627;  
 RA Endrizzi, M.G.; Hadinoto, V.; Grawney, J.D.; Miller, W.; Dietrich, W.F.;  
 RL "Genomic sequence analysis of the mouse Naip gene array.";  
 RL Genome Res. 10:1095-1102(2000).  
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
 CC DE BACULOVIRAL LAP REPEAT-CONTAINING PROTEIN 7 (NEURONAL APOPTOSIS  
 DE INHIBITORY PROTEIN 7).  
 DR BIRC1G OR NAIP7.  
 OC Mus musculus (Mouse).  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.  
 OX NCBI\_TAXID=10990;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20414747; PubMed=10958627;  
 RA Endrizzi, M.G.; Hadinoto, V.; Grawney, J.D.; Miller, W.; Dietrich, W.F.;  
 RL "Genomic sequence analysis of the mouse Naip gene array.";  
 RL Genome Res. 10:1095-1102(2000).  
 CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF  
 CC SIGNALS.  
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.  
 CC .....  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC .....  
 DR EMBL: AF242431; AAF82749.1; -.  
 DR EMBL: 06526; Birc1g.  
 DR InterPro: IPR001370; BIR.  
 DR Pfam: PF00653; BIR; 3.  
 DR SMART: SM00238; BIR; 3.  
 DR PROSITE: PS05043; BIR\_REPEAT\_1; 2.  
 DR PROSITE: PS01282; BIR\_REPEAT\_2; 3.  
 DR KW Apoptosis; Repeat; Multigene family.  
 FT REPEAT 60 127 BIR 1.  
 FT REPEAT 159 227 BIR 2.  
 FT REPEAT 278 345 BIR 3.  
 SQ SEQUENCE 1402 AA; 159662 MW; CIDFFBA359893E0D CRC64;

Query Match 15.2%; Score 498.5; DB 1; Length 1402;



Tue Jan 8 08:23:32 2002

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Search completed: January 7, 2002, 16:05:23  
Job time: 1402 sec